

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/530,987  
Source: PC  
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/530,987

DATE: 05/18/2006

TIME: 10:05:44

Input Set : A:\50125.101001.txt  
 Output Set: N:\CRF4\05182006\J530987.raw

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3 <110> APPLICANT: Dreher, Ingeborg
4       Moll, Thomas
6 <120> TITLE OF INVENTION: Antagonists IL-15
8 <130> FILE REFERENCE: 50125/101001
10 <140> CURRENT APPLICATION NUMBER: 10/530,987
11 <141> CURRENT FILING DATE: 2005-04-12
13 <150> PRIOR APPLICATION NUMBER: PCT/CH2003/00666
14 <151> PRIOR FILING DATE: 2003-10-13
16 <150> PRIOR APPLICATION NUMBER: EP 02022869.8
17 <151> PRIOR FILING DATE: 2002-10-14
19 <160> NUMBER OF SEQ ID NOS: 30
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 114
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapien
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34 Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
35           20          25          30
38 Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
39           35          40          45
42 Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
43           50          55          60
46 Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
47 65           70          75          80
50 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
51           85          90          95
54 Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
55           100         105         110
58 Thr Ser
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 231
64 <212> TYPE: PRT
65 <213> ORGANISM: Homo sapien
67 <400> SEQUENCE: 2
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73 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
74           20          25          30
77 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
78           35          40          45

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81 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
82      50          55          60
85 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
86 65          70          75          80
89 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
90          85          90          95
93 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
94          100         105         110
97 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
98          115         120         125
101 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
102 130          135         140
105 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
106 145          150         155         160
109 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
110          165         170         175
113 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
114          180         185         190
117 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
118          195         200         205
121 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
122          210         215         220
125 Leu Ser Leu Ser Pro Gly Lys
126 225          230
129 <210> SEQ ID NO: 3
130 <211> LENGTH: 232
131 <212> TYPE: PRT
132 <213> ORGANISM: Mus musculus
134 <400> SEQUENCE: 3
136 Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala
137 1          5          10          15
140 Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile
141          20          25          30
144 Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val
145          35          40          45
148 Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val
149          50          55          60
152 Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp
153 65          70          75          80
156 Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln
157          85          90          95
160 Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp
161          100         105         110
164 Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val
165          115         120         125
168 Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr
169          130         135         140
172 Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu
173 145          150         155         160

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176 Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr
177           165           170           175
180 Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr
181           180           185           190
184 Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr
185           195           200           205
188 Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys
189           210           215           220
192 Ser Phe Ser Arg Thr Pro Gly Lys
193 225           230
196 <210> SEQ ID NO: 4
197 <211> LENGTH: 346
198 <212> TYPE: PRT
199 <213> ORGANISM: artificial sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: fusion protein
204 <400> SEQUENCE: 4
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207 1           5           10           15
210 Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
211           20           25           30
214 Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
215           35           40           45
218 Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
219           50           55           60
222 Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
223 65           70           75           80
226 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
227           85           90           95
230 Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
231           100          105          110
234 Thr Ser Asp Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys
235           115          120          125
238 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
239           130          135          140
242 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
243 145           150          155          160
246 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
247           165          170          175
250 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
251           180          185          190
254 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
255           195          200          205
258 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
259           210          215          220
262 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
263 225           230          235          240
266 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
267           245          250          255

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270 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
 271 260 265 270  
 274 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
 275 275 280 285  
 278 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
 279 290 295 300  
 282 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
 283 305 310 315 320  
 286 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
 287 325 330 335  
 290 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 291 340 345  
 294 <210> SEQ ID NO: 5  
 295 <211> LENGTH: 347  
 296 <212> TYPE: PRT  
 297 <213> ORGANISM: artificial sequence  
 299 <220> FEATURE:  
 300 <223> OTHER INFORMATION: fusion protein  
 302 <400> SEQUENCE: 5  
 304 Asn Trp Val Asn Val Ile Ser Asp Leu Lys Thr Glu Asp Leu Ile  
 305 1 5 10 15  
 308 Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His  
 309 20 25 30  
 312 Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln  
 313 35 40 45  
 316 Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
 317 50 55 60  
 320 Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val  
 321 65 70 75 80  
 324 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile  
 325 85 90 95  
 328 Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn  
 329 100 105 110  
 332 Thr Ser Asp Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys  
 333 115 120 125  
 336 Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro  
 337 130 135 140  
 340 Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr  
 341 145 150 155 160  
 344 Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser  
 345 165 170 175  
 348 Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His  
 349 180 185 190  
 352 Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile  
 353 195 200 205  
 356 Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn  
 357 210 215 220  
 360 Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys  
 361 225 230 235 240

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Input Set : A:\50125.101001.txt

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364 Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu  
 365 245 250 255  
 368 Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe  
 369 260 265 270  
 372 Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu  
 373 275 280 285  
 376 Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr  
 377 290 295 300  
 380 Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg  
 381 305 310 315 320  
 384 Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His  
 385 325 330 335  
 388 Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys  
 389 340 345  
 392 <210> SEQ ID NO: 6  
 393 <211> LENGTH: 341  
 394 <212> TYPE: DNA  
 395 <213> ORGANISM: Homo sapien  
 397 <400> SEQUENCE: 6  
 398 aactgggtga atgtaataag tgatttggaaa aaaatttgaag atcttattca atctatgc 60  
 400 attgatgcta cttttatatac ggaaagtgtat gttcacccca gttgcaaagt aacagcaatg 120  
 402 aagtgcgttc tcttgaggat acaaggattt tcacttgagt ccggagatgc aagtattcat 180  
 404 gatacagtagt aaaatctgtat catccttagca aacaacagtt tgtcttctaa tgggaatgt 240  
 406 acagaatctg gatgcaaaga atgtgaggaa ctggaggaaa aaaatattaa agaattttg 300  
 408 cagagtttg tacatattgt ccaaattgttc atcaacactt c 341  
 411 <210> SEQ ID NO: 7  
 412 <211> LENGTH: 697  
 413 <212> TYPE: DNA  
 414 <213> ORGANISM: Homo sapien  
 416 <400> SEQUENCE: 7  
 417 cccaaatctg ctgacaaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 60  
 419 ggaccgtcag tcttccttccccccaaaa cccaaggaca ccctcatgtat ctcccggacc 120  
 421 cctgagggtca cgtcggtgggt ggtggacgtg agccacgaag accctgaggt caagttcaac 180  
 423 tggtaacgtgg acggcggtgg ggtgcataat gccaagacaa agccgcggga ggagcagtac 240  
 425 aacagcacgt accgtgtggt cagcgctcaccgtcaccgtcaccaggactg gctgaatggc 300  
 427 aaggagtaca agtgcaggt ctccaaacaaa gcccctccag ccccatcgaa gaaaaccatc 360  
 429 tccaaagcca aaggcagcc ccgagaacca caggtgtaca ccctgccccccatccggat 420  
 431 gagctgacca agaaccaggt cagcctgacc tgcctggta aaggcttcta tcccgacgac 480  
 433 atcgccgtgg agtggagag caatggccag ccggagaaca actacaagac cacgcctccc 540  
 435 gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtggca aagagcagg 600  
 437 tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 660  
 439 acccagaaga gcctctccct gtctccgggt aaatgtat 697  
 442 <210> SEQ ID NO: 8  
 443 <211> LENGTH: 700  
 444 <212> TYPE: DNA  
 445 <213> ORGANISM: Mus musculus  
 447 <400> SEQUENCE: 8  
 448 cccagaggcc ccacaatcaa gcccgtctt ccatgaaat gcccagcacc taaccttttg 60  
 450 ggtggaccat ccgtttcat cttccctcca aagatcaagg atgtactcat gatctccctg 120

**VERIFICATION SUMMARY**

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